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## Endocrine disorders associated with mutations in guanine nucleotide binding proteins

GRAEME MILLIGAN

Heterotrimeric guanine nucleotide binding proteins (G-proteins) play central roles in cellular information processing by allowing communication between heptahelical G-protein-coupled receptors and both enzymes which control the rate of production of intracellular second messengers and various classes of ion channels (Birnbaumer et al, 1990; Kaziro et al, 1991). The cellular level of cyclic adenosine monophosphate (cAMP) plays a key role in determining the growth rate of many cells (in either a positive or negative manner depending on the particular cell type) (Dumont et al, 1989; Burgering and Bos, 1995). As such, dysregulation of the control of cAMP production or degradation might be anticipated to result in changes in cellular growth control. Regulation of the activation of isoforms of protein kinase C has also been implicated in the regulation of cellular growth control. The activation status of certain members of this class of kinase is controlled by the production of *sn* 1-2 diacylglycerol derived via G-protein-linked receptor-catalysed hydrolysis of certain membrane phospholipids. Thus, a second endocrine-regulated G-protein-coupled pathway may contribute to cellular growth and differentiation (Seuwen and Pouyssegur, 1992). An analysis of human diseases, which result from mutations in individual G-proteins leading to dysregulation of these pathways, will form the basis of this chapter.

G-proteins consist of three non-identical, non-covalently associated subunits,  $\alpha$ ,  $\beta$  and  $\gamma$ . Approximately 20 distinct human G-protein  $\alpha$  subunits have now been identified. These are mainly the products of individual genes but in the cases of  $G_s$  (the G-protein responsible for receptor-mediated stimulation of adenylyl cyclase and thus of cAMP levels) and of  $G_o$  (a G-protein largely restricted to neural and endocrine tissues which functions to regulate the opening of voltage-operated  $Ca^{2+}$  channels) splice variation further increases the diversity. The  $\beta\gamma$  subunits exist physiologically as a non-dissociating complex and thus can be viewed as a single entity. These subunits are also present in multiple forms, with currently five  $\beta$  and seven  $\gamma$  subunit cDNA species having been identified. In the unactivated state the G-proteins exist as heterotrimeric complexes with the nucleotide binding pocket of the  $\alpha$  subunit being occupied by guanosine diphosphate (GDP). Upon hormone

occupation of a relevant receptor the rate of release of GDP from this site is increased markedly and subsequently it is replaced by guanosine triphosphate (GTP) (Bourne et al, 1990). The activated G-protein is then believed to physically dissociate into a GTP-liganded  $\alpha$  subunit and the  $\beta\gamma$  complex. Each of these complexes has the potential to regulate the activity of specific isoforms of effector enzymes. Inactivation of the GTP-bound G-protein is dependent upon the intrinsic GTPase activity of the  $\alpha$  subunit. This acts as a timer to limit temporally the active state and thus to prevent constitutive activation.

The activity of adenylyl cyclase is regulated directly by two sets of G-proteins. Stimulatory signals are transduced via the splice variants of  $G_s\alpha$  and inhibitory signals via the  $G_i$ -like G-proteins. Three related G-protein  $\alpha$  subunits,  $G_{i1}$ ,  $G_{i2}$  and  $G_{i3}$  can contribute to this in various situations but  $G_{i2}\alpha$  is generally regarded as the major inhibitory regulator (Simonds et al, 1989; McKenzie and Milligan, 1990).

The first indication that alterations in the structure of G-protein  $\alpha$  subunits could alter their activity and lead to the development of disease was the realization that the exotoxin of *Vibrio cholerae* possessed an adenosine diphosphate (ADP)-ribosyltransferase activity and that the  $\alpha$  subunit of  $G_s$  was the key cellular substrate for this activity. Ingestion of the cholera bacterium leads to sustained activation of adenylyl cyclase in cells of the intestinal epithelium, elevated levels of cAMP and subsequently transport of  $Cl^-$  ions and water from the cells. The effect of cholera toxin-catalysed ADP-ribosylation of  $G_s\alpha$  is to slow and indeed virtually eliminate the GTPase activity of the  $\alpha$  subunit (Bourne et al, 1990): therefore the G-protein becomes essentially constitutively active, resulting in maintained and hormone-independent activation of adenylyl cyclase. The target amino acid for cholera toxin-catalysed ADP-ribosylation of  $G_s\alpha$  is Arg201 and designed mutations at this position also result in constitutive activation of the G-protein (Freissmuth and Gilman, 1989). As this arginine is a key component of the regulatory turn-off mechanism of this G-protein it is not surprising that other G-protein  $\alpha$  subunits have an arginine residue at an equivalent position in their primary sequence. Although cholera toxin cannot modify this arginine in the majority of other G-proteins, designed mutations have shown that alterations in this position also result in constitutive activation. Such mutations have been enlightening in determining the downstream effector polypeptides which are regulated by individual G-proteins. A combination of these observations led to the concept that such mutations in these G-proteins might be responsible for, or contribute to, a variety of human endocrine disorders in which the normal regulation of cAMP production was abrogated.

### G-PROTEIN MUTATIONS IN AUTONOMOUS ENDOCRINE TUMOURS

Constitutive activation of adenylyl cyclase in the pituitary can result in cellular hyperplasia. The overproduction of pituitary-derived hormones

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was demonstrated by targeted transgenic expression of the enzymatically active subunit of cholera toxin in mice. This resulted in pituitary hyperplasia (presumably from the elevated cAMP levels) and gigantism (presumably via over-production of growth hormone) (Burton et al, 1991). Identification of a series of patients with growth hormone-secreting pituitary adenomas in which high basal adenylyl cyclase activity and poor responsiveness of the adenylyl cyclase to stimulatory agents such as growth hormone-releasing hormone (Vallar et al, 1987) suggested constitutive activation of the adenylyl cyclase cascade in cells of these tumours. Analysis of DNA derived from these tumours demonstrated that a considerable number of them harboured an activating mutation of  $G_s\alpha$  (Landis et al, 1989). These were clearly the result of somatic mutation as the mutant allele was not observed in genomic DNA isolated from peripheral blood cells, which contained only the wild-type sequence. Mutational alterations were found at two distinct codons: Arg201 and Gln227. As noted above, Arg201 is the site for cholera toxin-catalysed ADP-ribosylation. Gln227 is in a section of the primary sequence which comprises part of the guanine nucleotide binding pocket of the G-protein and is in an equivalent position to Gln61 in the small molecular mass G-protein p21 $ras$ . Mutation at this position in p21 $ras$  has been observed to result in activation of the protein and subsequent tumourigenesis in cells expressing such an allele (Bos, 1989). Subsequent studies have confirmed the presence of such activating mutations of  $G_s\alpha$  (often designated *gsp* mutations because of their oncogenic potential and the tradition of providing protein products of oncogenes with a simple three letter descriptor) in tumours from such patients (Clementi et al, 1990; Klibanski, 1990; Landis et al, 1990; Lyons et al, 1990; Spada et al, 1990; Drews et al, 1992; Adams et al, 1993; Yoshimoto et al, 1993; Tordjman et al, 1993).

These activating mutations of  $G_s\alpha$ , as might be anticipated, appear only to be associated with pituitary adenomas which display constitutive activity of adenylyl cyclase and not in those with normal regulation of this signalling cascade (Landis et al, 1989; Lyons et al, 1990). As the thyroid is also a tissue in which elevated cAMP levels is a growth stimulatory signal, equivalent mutations have been sought and identified in some autonomously functioning thyroid adenomas (Lyons et al, 1990; O'Sullivan et al, 1991) and a limited number of thyroid carcinomas (Suarez et al, 1991). No reports of activating mutations of  $G_s\alpha$  associated with melanomas or tumours of the adrenal cortex have appeared, even though these tissues contain cell types in which cAMP is a positive growth stimulus. To date, the only other equivalent mutations reported for a G-protein  $\alpha$  subunit associated with human disease have been Arg179 (the position equivalent to Arg201 in  $G_s\alpha$ ) mutations in  $G_{12}\alpha$  in small numbers of adrenal medulla ovarian tumours (Lyons et al, 1990). This association has led to the mutant  $G_{12}\alpha$  proteins being named *gip2* to indicate its oncogenic potential in a similar manner to the use of *gsp* for the activating mutations of  $G_s\alpha$ .

Although not a mutant protein, Selzer et al (1993) have noted that the expression of  $G_{12}\alpha$  is tightly regulated in vivo and in primary cultures of

thyroid epithelial cells by thyrotrophin. This regulation is lost in autonomous adenomas of the thyroid where  $G_{\beta 1}$  is expressed independently of the presence of thyrotrophin. The contribution of this G-protein to the development of the condition, however, is not currently clear.

### ALBRIGHT HEREDITARY OSTEODYSTROPHY

Albright hereditary osteodystrophy (AHO) is a disorder inherited as an autosomal dominant and is identified clinically by short stature, obesity, subcutaneous ossifications, focal skeletal defects and rounded facies. When associated with resistance to a range of hormones which function via  $G_{\alpha}$  to raise intracellular concentrations of cAMP (e.g. parathyroid hormone, luteinizing hormone, glucagon) it is termed pseudohypoparathyroidism type 1a (PHP 1a). The observation of AHO without PHP 1a in relatives of these patients is described as pseudopseudohypoparathyroidism (PPHP). Membranes from a variety of tissues of many AHO patients show a reduction of approximately 50% compared to control, in functional  $G_{\alpha}$  activity as measured by reconstitution of adenylyl cyclase activity to membranes of S49 cyc<sup>-</sup> cells (which genetically lack  $G_{\alpha}$ ) by detergent extracts of membranes from the tissues of the patients. Levels of each of  $G_{\alpha}$  protein, measured by immunoblotting (Patten and Levine, 1990), and  $G_{\alpha}$  mRNA, as detected by Northern blots (Carter et al, 1987; Levine et al, 1988), are also substantially reduced (although levels of this mRNA are not reduced in all kindreds). Reduced levels of  $G_{\alpha}$  activity have also been noted in PPHP patients (Levine et al, 1986). It is thus unclear what other alterations must be manifest to result in the clinical phenotype of AHO with PHP 1a. Speculation has centred on other elements of the cellular cAMP generation and degradation machinery such as cAMP phosphodiesterases (Spiegel, 1990), but no data to support such a contention are currently available.

By contrast, patients with isolated resistance to parathyroid hormone in the absence of AHO (termed pseudohypoparathyroidism type 1b), have normal immunologically detectable cellular levels of  $G_{\alpha}$  (Patten and Levine, 1990). Such patients may have defects in the parathyroid hormone receptor (Silve et al, 1986). Clearly, a variety of genetic alterations could be responsible for the reduced tissue levels and activity of  $G_{\alpha}$  associated with AHO and the differences between kindreds in levels of relevant mRNA. Genetic analysis has indeed proved this to be the case (Patten et al, 1990; Weinstein et al, 1990; Lin et al, 1992; Weinstein et al, 1992; Miric et al, 1993; Schwindinger et al, 1994; see Miric and Levine, 1992 for review). The first mutation noted in the  $G_{\alpha}$  gene associated with some AHO patients was a single base substitution in one allele resulting in the conversion of the initiator codon ATG (methionine) to GTG (valine) (Patten et al, 1990). The normal 45 kDa  $G_{\alpha}$  in membranes of erythrocytes of these patients was substantially reduced compared to controls. However, an apparent 77 kDa polypeptide containing immunological information consistent with the presence of a C-terminal  $G_{\alpha}$  epitope but not an N-terminal region was observed. While one hypothesis would have anticipated the

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## DDYSTROPHY

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appearance of a truncated form of the G-protein resulting from initiation from an internal, in frame, AUG codon, no shorter species corresponding immunologically to  $G_{\alpha}$  were observed (Patten et al, 1990). The nature of the 77 kDa polypeptide, however, remains to be fully explored. A considerable range of other mutations in individual AHO kindreds have now been shown. These include a G to C substitution at the donor splice junction of intron 10 of the  $G_{\alpha}$  gene (Weinstein et al, 1990), which would be anticipated to result in abnormal RNA splicing; a coding frameshift created by a single base deletion within exon 10 (Weinstein et al, 1990) and a single amino acid mutation (R385H) (Schwindinger et al, 1994) close to the C-terminus of  $G_{\alpha}$ . This mutation is in a region known to be involved in contacts between receptors and  $G_{\alpha}$  as  $\beta 2$ -adrenoceptor contact with  $G_{\alpha}$  is abolished in lymphoma S49 *unc* cells which harbour a R389P mutation in  $G_{\alpha}$  (Sullivan et al, 1987).

## McCUNE-ALBRIGHT SYNDROME

The McCune-Albright syndrome is an interesting example of mosaicism. This mechanism was first suggested by Happle (1986) in view of the multi-site tissue abnormalities and the observed patterns of hyperpigmentation in this disorder. The condition is defined classically by the presence of cutaneous hyperpigmentation, polyostotic fibrous dysplasia and a range of endocrine hyperfunctions of varying degrees in systems anticipated to be coupled to the stimulation of adenylyl cyclase. As the endocrinopathies may include sexual precocity and autonomous adrenal hyperplasia, and the unusual 'café au lait' pigmentation arises from excess functioning of melanocytes, then it was reasonable to suggest that the condition might result from over-activity of the adenylyl cyclase cascade. Furthermore, the bone lesions associated with the disorder resemble those that occur in primary hyperparathyroidism. As with the examples of pituitary and thyroid adenomas discussed above, patients with McCune-Albright syndrome harbour activating mutations (*gsp*) of the  $G_{\alpha}$  gene. Weinstein and Shenker (1993) and Weinstein et al (1991) have reported the identification of Arg201 mutations of  $G_{\alpha}$  in tissues from 15 McCune-Albright syndrome patients and others have reported equivalent mutations (Schwindinger et al, 1992). DNA extracted directly from a 'café au lait' patch of skin has also been shown to contain the activating  $G_{\alpha}$  mutation (Schwindinger et al, 1992). As the presence of the mutated allele could not be shown in all tissues, and to variable extents in tissues displaying its presence, such data support the notion of mosaicism.

The mosaicism in McCune-Albright syndrome has been suggested to occur as the result of a post-zygotic somatic cell mutation (Happle, 1986). This would account appropriately for the lack of genetic inheritance of the condition (perhaps due to lethality of an equivalent germ line mutation) and the variability in degree and distribution of the endocrine abnormalities in affected individuals. Furthermore, as cAMP is growth inhibitory in a wide range of tissues, malignancy is uncommon in the condition.

## TESTITOXICOSIS

Leydig cells of the testis are stimulated to produce the androgen testosterone by the action of luteinizing hormone (LH). LH, produced by the anterior pituitary, binds to and activates a specific heptahelical G-protein-coupled receptor leading to the activation of  $G_s\alpha$  and adenylyl cyclase and thus elevation of intracellular cAMP levels. Potential activating mutations in the LH receptor pathway might be anticipated to lead to constitutive production of testosterone and thus to the development of cases of testitoxicosis or familial male precocious puberty. As with other G-protein-linked signalling cascades, such alterations could potentially be produced by mutation of receptor, G-protein or adenylyl cyclase. Strong linkage of a single base alteration (A→G), resulting in substitution of Gly 578 in the putative sixth transmembrane helix by aspartate, has been reported in a study of eight different families with gonadotrophin-independent generation of testosterone and Leydig cell hyperplasia in the presence of prepubertal levels of circulating LH (Shenker et al, 1993). Transient expression in COS cells of an LH receptor cDNA mutated in this position resulted in elevated production of cAMP in the absence of agonist (Skenker et al, 1993), demonstrating this mutation to result in constitutive activation of the adenylyl cyclase cascade. Clearly, an activating mutation of  $G_s\alpha$  similar to those observed in pituitary adenomas (see above) would be expected to result in a similar phenotype.

Examination of two unrelated boys with an apparently paradoxical mixture of testitoxicosis and pseudohypothyroidism type 1a (Nakomoto et al, 1993) led to the detection of a novel activating mutant of  $G_s\alpha$  with a number of intriguing features which are seemingly able to account for this unexpected combination of features (Iiri et al, 1994). In these patients a mutation in the  $G_s\alpha$  gene resulted in the replacement of Ala 366 by serine (A366S) (Iiri et al, 1994). To examine how such a mutation in  $G_s\alpha$  could result in an apparent gain of G-protein function in the testis but be consistent with the apparent reduction of function in other tissues, an A366S mutant  $G_s\alpha$  cDNA was constructed (incorporating an epitope tag for easy immunological detection) and compared to the epitope-tagged wild-type G-protein in a range of assays. The purified mutant protein was shown to bind the poorly hydrolysed analogue of GTP, [ $^{35}$ S]GTP $\gamma$ S, much more rapidly than the wild-type protein. However, with prolonged incubation the maximal level of binding was not different (Iiri et al, 1994). This difference reflected a markedly elevated rate of release of bound GDP (which is normally the rate-limiting step for guanine nucleotide exchange) by the A366S mutant. As such, in the cells of the patient it would be anticipated that the mutant protein would spend a greater fraction of its time in the GTP-bound and hence activated state leading to constitutive activation of adenylyl cyclase. However, while consistent with the clinical gain of function features of testitoxicosis this is apparently not consistent with the anticipated loss of function features of pseudohypothyroidism type 1a. When expressed in cultured cells grown at 37°C the A366S mutant  $G_s\alpha$  protein was shown to be much less stable than the wild-type protein, thus leading to its rapid degradation.

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## LACK OF ASSOCIAT

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Such differential rates of degradation were not observed at 33°C. It is thus likely that in the patients, at the temperature of the testis, the mutant protein was relatively stable and thus could function as a mutant capable of producing constitutive activation of adenylyl cyclase. It may be that steady-state levels of the mutant protein in other tissues of the body are low due to the short half-life of the protein, such that the level of expressed protein, while still constitutively active, is insufficient to produce even a normal level of adenylyl cyclase activation. However, it should be noted in the cellular transfection experiments reported by Iiri et al (1994) that the levels of the A336S  $G_s\alpha$  mutant achieved following transfection, whilst lower than that of wild-type protein, was sufficient to cause a greater elevation of cAMP levels than that produced by the wild-type protein. It thus requires further analysis of levels and function of the mutant  $G_s\alpha$  protein in such patients to confirm that the reported clinical phenotype can be explained solely on the basis of this single mutation.

### LACK OF MUTATIONS IN OTHER G-PROTEINS ASSOCIATED WITH ENDOCRINE DISORDERS

To date there have been no reports of gain or loss of function in endocrine disorders resulting from mutations in members of families of heterotrimeric G-protein  $\alpha$  subunits apart from  $G_s\alpha$  and  $G_{12}\alpha$  (and, as noted above, those associated with a  $G_{12}\alpha$  mutation are extremely limited). At first sight, this is a surprise as the generation and expression of constitutively activating mutant cDNA species of members of the  $G_i/G_{11}$  and  $G_{12}$  families of G-proteins (which are widely expressed) have been reported to result in alterations of growth control (both positive and negative) and in some cases in transformation of fibroblast cell lines. For example, it has been reported that the GTPase deficient mutation of  $G_q\alpha$  ( $G_q\alpha$  Q209L) can cause transformation of NIH 3T3 cells (Kalinec et al, 1992; De Vivo et al, 1992). However, such observations are not universal: Wu et al (1992) found this mutant to be growth inhibitory to NIH 3T3 cells. Expression of many of these mutants results in a strong agonist-independent activation of phospholipase  $C\beta$  activity and certainly many G-protein-linked receptors for mitogens activate members of the  $G_q$ -family of G-proteins (Wu et al, 1992; Qian et al, 1994) leading to stimulation of phospholipase  $C\beta$  activity. Such results clearly indicate that activation of phospholipase  $C\beta$  is an insufficient indicator of mitogenic potential. Many G-protein-linked mitogenic ligands which do activate phospholipase  $C\beta$  also regulate a variety of other enzyme cascades including phospholipase A2 and the MAP kinases. A number of receptors for other G-protein-linked mitogenic ligands interact with  $G_{12}\alpha$  (van Corven et al, 1993; Winitz et al, 1993; Alblas et al, 1993). These may produce their regulation of mitogenesis either by provision of G-protein  $\beta\gamma$  subunits (Crespo et al, 1994; Faure et al, 1994; Koch et al, 1994), which directly or indirectly lead to activation of MAP kinases, or by reduction of cellular cAMP levels (Sevetson et al, 1993; Hordijk et al, 1994). Mutational activation of  $G_{12}\alpha$  has also been reported



to be highly oncogenic when expressed in NIH 3T3 cells (Xu et al, 1993; Jiang et al, 1993). The lack of identified mutations in human disease in these other G-proteins equivalent to the *gsp* and *gip2* mutations discussed above is thus somewhat surprising and the reasons for this remain to be clearly elucidated.

## SUMMARY

The basis for a number of relatively rare endocrine diseases, which present clinically with features of AHO, have been shown conclusively to result from mutations in the  $G_{\alpha}$  gene which interfere with the expression of functional protein. Individual kindreds display a range of specific mutations in this gene. A further series of disorders result from somatic mutations of the  $G_{\alpha}$  gene which result in constitutive activation (in one case probably with a concomitant decrease in stability of the expressed protein). When such a mutation occurs in early embryogenesis it can result in a pattern of mosaicism of expression of clinical features in the patient. Despite these cases, equivalent alterations in other G-protein  $\alpha$  subunit genes seem to be of limited importance in human disease. This is despite biochemical data from a range of experimental cell models which indicate that such mutations can have potent effects on cell growth and division.

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